5. (Amended) Method according to claim 1, further characterized in that genomic DNA of several individuals, tissues, cell lines or cells is amplified separately and then treated jointly according to step e) of claim 1.

6. (Amended) Method according to claim 1, further characterized in that by formation of heteroduplexes from the DNA of different individuals, tissues, cell lines or cells, erroneous base pairings are produced at the positions at which a 5-methylcytosine was localized in the genomic DNA.

9. (Amended) Method according to claim 6, further characterized in that the erroneous base pairings by means of "chemical mismatch cleavage" (chemical modification at non-complementary positions) lead to a specific or sufficiently selective backbone cleavage at these positions.

10. (Amended) Method according to claim 6, further characterized in that the DNA is cleaved enzymatically specifically or sufficiently selectively at the erroneous base pairings.

11. (Amended) Method according to claim 1, further characterized in that DNA fragments are obtained in step e) according to claim 1, whose size infers the cleavage positions and thus the position of methylcytosines and/or the methylation positions that differ between different individuals, tissues, cell lines or cells.

15. (Amended) Method according to claim 13, further characterized in that the size of the fragments produced in step e) according to claim 1 is adapted to the performance capacity of the mass spectrometer.

18. (Amended) Method according to claim 1, further characterized in that in step b) one primer of the PCR is provided with a chemical function, so that the PCR product can be immobilized on a surface.

19. (Amended) Method according to claim 1, further characterized in that the PCR product produced in step b) is transferred to different reaction vessels and the surfaces of the reaction vessels are chemically treated such that the PCR product can be bound thereon.

20. (Amended) Method according to claim 1, further characterized in that PCR products of different individuals that are produced in step c) are transferred into different reaction vessels the surfaces of which are chemically treated such that the PCR product can be bound thereon.

21. (Amended) Method according to claim 1, further characterized in that an enzyme which forms a complex with a non-complementary base pair is used for step e).

25. (Amended) Method according to claim 1, further characterized in that one compares an amplified DNA sample according to step c) in claim 1, which displays a difference relative to an amplified DNA sample in step b), in a second run of the method itself, with a similar DNA sample according to step b) in claim 1 and with all other DNA samples to be investigated.

26. (Amended) Method according to claim 1, further characterized in that a preselection of gene segments to be investigated in detail by the mass spectrometer is conducted by means of fluorescence labeling or chemiluminescence labeling of the immobilized DNA strand, the lack of which, after conducting steps d) and e) of claim 1 and a washing step, indicates the presence of methylated cytosines in the investigated genomic DNA segment.

27. (Amended) Method according to one of claims 1 to 25, further characterized in that a preselection is made of the gene segments to be investigated in detail by mass spectrometry by means of a more non-specific variant.